Amendments to the claims:

1. (Currently Amended) A method for ~~screening for~~ identifying a transcription factor modulator ~~modulators~~, the method comprising:

~~forming a plurality of test samples by contacting samples of cells with different agents; and~~

~~for each test sample, identifying which of a plurality of different activated transcription factors are present by taking~~

treating a sample of cells with a test agent, the treated sample forming the test sample,

providing a library of double stranded nucleic acid probes, the nucleic acid probes each comprising a recognition sequence ~~that is known to bind to an activated known transcription factor and varies within the library for binding to different activated known transcription factors~~ varying within the library and the nucleic acid probes in the library being capable of binding to at least two activated transcription factors selected from the group consisting of AP1, AP-2, ARE, Brn-3, C/EBP, CBF, CDP, c-Myb, CREB, E2F-1, EFR, ERE, Ets, Ets-1/PEA3, FAST-1, GAS/ISRE, GATA, GRE, HNF-4, IRF-1, MEF-1, MEF-2, Myc-Max, NF-1, NFATc, NF-E1, NF-E2, NF.kappa.B, Oct-1, p53, Pax-5, Pbx1, Pit 1, PPAR, PRE, RAR, RAR (DR-5), SIE, Smad SBE, Smad3/4, SP1, SRE, Stat1, Stat3, Stat4, Stat4, Stat5, Stat6, TFIID, TR, TR(DR-4), USF-1, VDR (DR-3), HSE, and MRE,

contacting the test sample with the library of double stranded ~~DNA~~ nucleic acid probes under conditions where nucleic acid probe - transcription factor complexes are formed between the nucleic acid probes and activated transcription factors present in the test sample,

isolating the nucleic acid probes from the nucleic acid probe-transcription factor complexes formed,

contacting the isolated nucleic acid probes with an array of immobilized hybridization probes under conditions suitable for hybridization of the strands of the different double stranded nucleic acid probes to the hybridization probes in the array, wherein identification of the nucleic acid probes bound to the array determines which of the activated transcription factors are present in the test sample, and

comparing the activated known transcription factors present in the test sample with the activated known transcription factors present in a control sample of cells not contacted with the test agent ~~any of the different agents~~, the difference in the presence of transcription factors

between the test and control sample being indicative of the transcription modulation by the agent contacted with the test sample~~; and~~

~~comparing the activated transcription factors present in the different test samples~~.

2. (Previously Presented) The method according to claim~~s~~ 1 wherein each of the double stranded nucleic acid probes in the library has a recognition sequence greater than 35 base pairs in length.

3. (Previously Presented) The method according to claim~~s~~ 1 wherein each of the double stranded nucleic acid probes in the library has a recognition sequence greater than 40 base pairs in length.

4. (Previously Presented) The method according to claim~~s~~ 1 wherein each of the double stranded nucleic acid probes in the library has a recognition sequence greater than 45 base pairs in length.

5-7. (Canceled)

~~8~~. (Previously Presented) The method according to claim~~s~~ 1 wherein each of the recognition sequences has between 20 and 40 base pairs in length.

~~9~~. (Previously Presented) The method according to claim~~s~~ 1 wherein each of the recognition sequences has between 25 and 35 base pairs in length.

~~10~~. (Previously Presented) The method according to claim~~s~~ 1 wherein the library of double stranded nucleic acid probes comprises at least 5 different nucleic acid probes each having a different recognition sequence.

~~11~~. (Previously Presented) The method according to claim~~s~~ 1 wherein the library of double stranded nucleic acid probes comprises at least 10 different nucleic acid probes each having a different recognition sequence.

9

12. (Previously Presented) The method according to claims 1 wherein the library of double stranded nucleic acid probes comprises at least 20 different nucleic acid probes each having a different recognition sequence.

10

13. (Previously Presented) The A method according to claims 1 wherein the library of double stranded nucleic acid probes comprises at least 50 different nucleic acid probes each having a different recognition sequence.

11

14. (Previously Presented) The method according to claims 1 wherein the recognition sequences in the library of nucleic acid probes are for recognizing activated transcription factors from at least 5 different types of cells.

12

15. (Previously Presented) The A method according to claims 1 wherein the recognition sequences in the library of nucleic acid probes are for recognizing activated transcription factors from at least 10 different types of cells.

13

16. (Previously Presented) The method according to claims 1 wherein the recognition sequences in the library of nucleic acid probes are for recognizing activated transcription factors from malignant, benign, and normal cell types.

14

17. (Previously Presented) The method according to claims 1 each of the immobilized hybridization probes on the array comprises at least two copies of a complement to a portion of a recognition sequence comprised on the nucleic acid probe.

18. (Canceled)

15

19. (Previously Amended) The method according to claim 1, wherein the recognition sequences comprised on the nucleic acid probes are known to bind to two or more transcription factors selected from the group consisting of NF-E1, NFκB, Ets, Ap1, p53 and c-Myb.